

O114

2-hour Oral Session

MDR Enterobacteriaceae: clinical epidemiology and outcomes

Colonization rates and risk factors for extended-spectrum beta-lactamase producing coliforms (ESBLPCs) in different sections of the asymptomatic general population in England

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Background: ESBLPCs are common in the gut of populations where antibiotics are over used. Most prevalence data comes from patients with diarrhoea. We aimed to estimate how many of the general population in England carry ESBLPCs and determine independent risk factors for their presence.

Material/methods: Patients 18+ from 15 practices in four Primary Care Trusts (PCTs) with different ethnicity across England were stratified by antibiotic use, gender and ethnicity. Randomly selected patients were invited by letter and returned a stool sample and questionnaire. Stools were cultured directly on selective chromogenic agar, and MALDI-TOF mass spectrometry was used to determine bacterial species; multiplex PCR and sequencing was used to determine presence of the *bla*_{CTX-M} gene and genotype. Second specimens were collected from a subset. We used 2011 census data, practice population and return rate to give a weighted prevalence of ESBLPCs, and used multivariate analysis to explore risk factors.

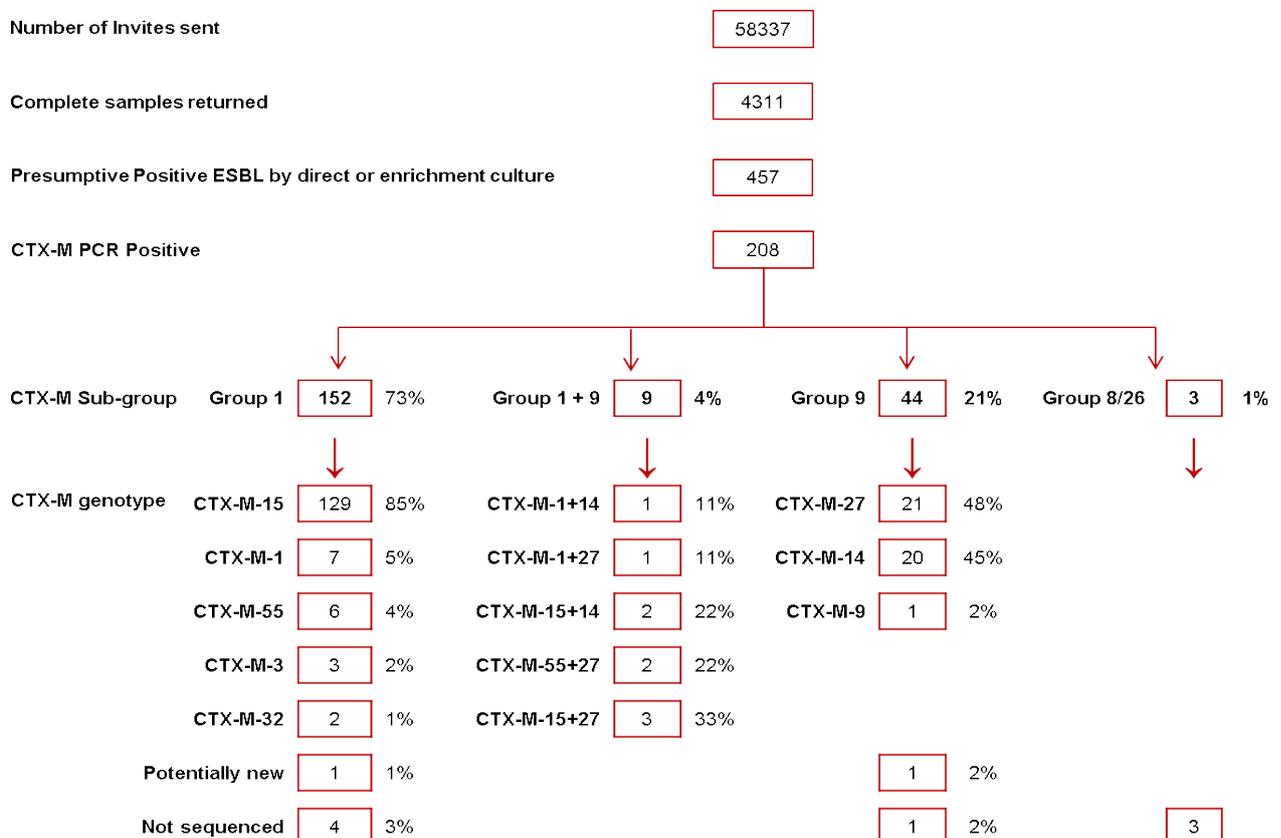
Results: 2296 (3.9%) of 58,337 returned a stool and questionnaire; 2171 patients (Birmingham 205, London 534, Southampton 699, Shropshire 733) are included in the weighted analysis.

Prevalence: The estimated overall prevalence of *bla*_{CTX-M}ESBLPCs among adults usually resident in England in 2014 was 7.3% [CI5.6, 9.4]. There was a significant difference by PCT: Birmingham 16%, London 12.7%, Southampton 11.3%, Shropshire 4.9% (p=0.002). Country of birth was the most important factor determining prevalence: born in the UK 6.5% *versus* 15.8% if born outside the UK, p<0.001; Indians (28%), Pakistanis(19%), Bangladeshi(26%) and Sri Lankans(13%) had significantly higher prevalence.

Risk Factors adjusted for country of origin: Hospitalisation (OR 3.8) or diarrhoea while abroad in the last year (OR 1.8), and travel outside the UK to countries in the Indian subcontinent (OR 3.4), Africa (OR 2.1) the Middle East (OR 2.1) and South or Central America (OR 3.0), South East or Pacific Asia (OR3.0), Africa (OR 2.1), Middle East (OR 2.1) and South or Central America (OR3.0) were significant risk factors for *bla*_{CTX-M}ESBLPCs. Travel to other areas, GP practice, age, gender, practice antibiotics, diet, healthcare work, hospitalisation in UK, animal contact, number in patient's household, number of children or pets were not risk factors.

44% of 133 initially positive for *bla*_{CTX-M} ESBLPCs were still positive at follow up; (1-2m 59%; 5-10m 39%, 9% decrease /month). 4% of 205 individuals initially negative were positive at follow up, with no significant risk factors.

Determination of *bla*_{CTX-M} groups:



Conclusions: These findings have considerable implications for UK healthcare as they demonstrate there is a large faecal reservoir of ESBL genes in defined sections of the population, with prolonged carriage. Travel to certain countries also puts individuals at risk. The high rate of CTX-M-27 is unusual in the UK and has previously only been reported at a low frequency from food animals.